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CLAIMS

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1. A process for purification of a heterologous protein of interest, comprising
 - 5 (a) providing a fusion protein comprising said heterologous protein fused to a CBM intercepted by a proteolytic cleavage site,
 - (b) contacting said fusion protein with a functional protease fused to a CBM , at conditions facilitating proteolytic cleavage by said protease, to cleave the CBM from the heterologous protein of interest,
 - 10 (c) contacting the solution of CBM-protease, free CBM and heterologous protein of interest to a polysaccharide matrix, under conditions where the CBM-protease and free CBM binds to said polysaccharide matrix and where the heterologous protein of interest is not retained on said polysaccharide matrix,
 - (d) separating the non-bound heterologous protein of interest from the polysaccharide matrix,
 - 15 (e) washing the polysaccharide matrix with the bound CBM-protease and CBM, with one or more suitable aqueous solutions,
 - (f) eluting the CBM-protease from the matrix by adjusting conditions effecting the release of said CBM-protease off the matrix; and
 - 20 (g) optionally reconditioning said eluted CBM-protease, to retain its affinity to said polysaccharide matrix, such that the reconditioned CBM-protease can be re-used for subsequent repetition of the process defined by steps (a) – (g) wherein said CBMs are capable of binding reversibly to a polysaccharide matrix and being released from such matrix by non-denaturing elution conditions and
 - 25 do not bind substantially to insoluble cell-wall plant material, the method.
2. The process of claim 1, wherein said protease fused to CBM is from the group of proteases consisting of enterokinase, tobacco etch virus (TEV) protease, factor X and thrombin.
- 30 3. The process of claim 2 wherein said protease is mammalian enterokinase (EK) or an enterokinase active part thereof.
4. The process of claim 3, wherein said EK comprises a bovine EK catalytic domain (EKc).
- 35 5. The process of claim 4, wherein said bovine EKc is encoded by the nucleic acid sequence shown as SEQ ID NO: 2.